3. Claims 9, 10, 22, 28 and 56 stand rejected for lack of patentable utility (§101) lack of enablement (112/1), and lack of description (112/1). Claims 9, 10 and 56 have been cancelled.

Claim 22 is to a pharmaceutical composition comprising the polypeptide of claim 1. Claim 28 is to the method of using that polypeptide to treat patients deficient in MASP-2.

Deficiency in MASP-2 activity is a specific medical condition and we therefore disagree with the examiner that no specific medical condition is disclosed. A case report on a patient suffering from MASP-2 activity deficiency is described in the enclosed declaration.

Hence, we disagree with the examiner and respectfully request said claims be allowed.

4. Claims 1-10, 22, 28 and 47-56 are rejected for lack of description. In essence, the issue is one of "effective description", i.e., of a sufficient structural relationship to disclosed sequences IDs 1 and 2 so the latter are representative of the entire genus claimed.

Claim 4 requires a polypeptide comprising SEQ ID NO:1. While there is no limitation on the flanking sequence, if ID 1 is the active site, this claim seems justifiable under the written description training materials. We refer specifically to Example 13, claim 1 of the materials ("An isolated protein having SEQ ID NO:3).

Claims 5 and 6 add MW limitations. A 20K protein would be about 200 a.a. A 52K protein would be about 520 a.a. SEQ ID NO:1 is 41 a.a., while ID 2 is 686 a.a.

Claims 47 and 49-52 define allowed mutants by overall percentage identity with SEQ ID NO:2 (85%-99%), while 48 refers to ID1 (85%). Claims 47-52 are justifiable under the written description training materials (WDTM). We refer specifically to Example 14 of the WDTM: "A protein having SEQ ID NO:3 and variants thereof that are at least 95% identical to SEQ ID NO:3

and catalyze the reaction of A→B". Claim 50, like the WDTM example, recites 95%. However, the WDTM did not exclude lower percentages.

Claims 53 and 54 further limit claims 47 and 48, respectively, in terms of the nature of the substitutions.

5. The enablement rejections of claims 1-7 and 47-55 relate to the possible mutations of the sequence.

Claims 1, 2, 3 and 7 have been cancelled. Claims 4-6 require the presence of SEQ ID NO:1. Hence, they do not allow mutation within SEQ ID NO:1.

Claims 47 to 55 relate to functional MASP-2 peptides sharing a certain percentage of identity with the specifically disclosed MASP-2 sequences.

The Examiner finds that the specification does not describe how MASP-2 peptides according to claims 47 to 55 may be prepared. However, it is common within the art to prepare mutants of polypeptides with similar function either randomly (see description p. 28, l. 31) or by site directed mutagenesis (see description p. 29, l 2-4). It is generally accepted in the art that some amino acids within a polypeptide may be exchanged for other amino acids without changing the function of said polypeptide. In particular, it is frequently possible to exchange amino acids with amino acids with similar functions, i.e. conservative substitutions and still retain the function of a polypeptide (description p. 10, l. 15-24) as cited in claim 53 and 54. In the specification it is also described that conserved and variable positions within the peptide sequence should be distinguished and that conserved residues preferably are not altered. Conserved residues may for example be identified by aligning MASP-2 sequences (description p. 29, l. 8-15). However it will be apparent to a person skilled in the art that alignments of SEQ ID NO:1 and 2 with other serine proteases may also be used to identify conserved positions. Figure 6 shows an

alignment of MASP-2 to MASP-1, C1r and C1s. Amino acids conserved in all 4 proteins are indicated by asterisks. Domains within the proteins are indicated, in particular, is the serine protease domain indicated together with the specific positions within said domain required for the active centre (see also description p. 48, l. 28 to p. 49, l. 9). Hence, in our opinion the specification indeed discloses how to prepare mutants of MASP-2 as claimed in claim 47 to 55.

In addition, a naturally occurring MASP-2 mutation, which has no effect on the function of MASP-2 has been identified as described in the enclosed affidavit.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

Respectfully submitted,

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Enclosure
-Declaration

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the claims:

Claims 11, 41-45, 47 and 55 have been amended as follows:

11 (twice amended). A [The] polypeptide with a molecular mass of about 52K [according to claim 5 or claim 6], said polypeptide having the amino acid sequence of SEQ ID NO:2.

41 (amended). A [The] polypeptide [of claim 40 in which the fragment of SEQ ID NO:2 is] comprising a fragment of SEQ ID NO:2, wherein said fragment is at least 20 amino acids in length.

42 (amended). The polypeptide of claim [40] 41 in which the fragment of SEQ ID NO:2 is at least 25 amino acids in length.

43 (amended). The polypeptide of claim [40] 41 in which the fragment of SEQ ID NO:2 is at least 35 amino acids in length.

44 (amended). The polypeptide of claim [40] 41 in which the fragment of SEQ ID NO:2 is at least 50 amino acids in length.

45 (amended). The polypeptide of claim [40] 41 in which the fragment of SEQ ID NO:2 is at least 100 amino acids in length.

47 (amended). A polypeptide comprising a sequence at least 85% identical to SEQ ID NO:2
wherein said polypeptide has at least one of the following activities

i) MASP-2 activity in an in vitro assay for MBLectin complement pathway function; or

ii) serine protease activity; or

iii) mannan-binding lectin (MBL) associating activity.

55 (amended). The polypeptide of any one of claims [40-54] 41-46, 48, 54 in which the polypeptide is characterized by at least one of the following activities:

a. ability to associate with mannan-binding lectin;

b. serine protease activity or cleavage of complement factor C2 or C4;

c. MASP-2 activity in an in vitro assay for MBLectin

complement pathway function;

d. competitive inhibition of one of a.-c. above.

Claims 1, 2, 3, 7, 8, 9, 10, 40 and 56 have been cancelled.